Amendments to the Specification:

Insert the paper copy of the substitute sequence listing filed herewith.

At page 1, after the title, please insert the following paragraph:

Cross Reference to Related Applications

This application claims priority to and is a divisional application of U. S. Application Serial No. 09/995,297, filed November 27, 2001, which is a divisional application of U. S. Application Serial No. 09/128,602, filed August 3, 1998, both of which are hereby incorporated herein by reference in their entirety for all purposes.

Please amend the paragraph beginning at page 5, line 6, as follows:

Figure 2 shows the nucleotide sequences for a *Brassica* Fad2-D wild type gene (Fad2-D wt; SEQ ID NO:9), IMC129 mutant gene (Fad2-D GA316 IMC129; SEQ ID NO:11), Fad2-F wild type gene (Fad2-F wt; SEQ ID NO:13), Q508 mutant gene (Fad2-F TA515 Q508; SEQ ID NO:15) and Q4275 mutant gene (Fad2-F GA908 Q4275; SEQ ID NO:17).

Please amend the paragraph beginning at page 5, line 10, as follows:

Figure 3 shows the deduced amino acid sequences (SEQ ID NOS:10, 12, 14, 16, and 18) for the polynucleotides of Figure 2.

Please amend the paragraph beginning at page 9, line 8, as follows:

Preferred mutations are in a region of the nucleic acid encoding an amino acid sequence motif that is conserved among delta-12 fatty acid desaturases or delta-15 fatty acid desaturases, such as a His-Xaa-Xaa-Xaa-His motif (Tables 1-3). An example of a suitable region has a conserved HECGH motif (SEQ ID NO:60) that is found, for example, in nucleotides corresponding to amino acids 105 to 109 of the *Arabidopsis* and *Brassica* delta-12 desaturase sequences, in nucleotides corresponding to amino acids 101 to 105 of the soybean delta-12

desaturase sequence and in nucleotides corresponding to amino acids 111 to 115 of the maize delta-12 desaturase sequence. See e.g., WO 94/15116; Okuley et al., Plant Cell 6:147-158 (1994). The one letter amino acid designations used herein are described in Alberts, B. et al., Molecular Biology of the Cell, 3rd edition, Garland Publishing, New York, 1994. Amino acids flanking this motif are also highly conserved among delta-12 and delta-15 desaturases and are also suitable candidates for mutations in fragments of the invention.

Please amend the paragraph beginning at page 9, line 21, as follows below. Please note that the underlining in HECGH and HKCGH is in the original application.

An illustrative embodiment of a mutation in a nucleic acid fragment of the invention is a Glu to Lys substitution in the HECGH motif (SEQ ID NO:60) of a *Brassica* microsomal delta-12 desaturase sequence, either the D form or the F form. This mutation results in the sequence HECGH (SEQ ID NO:60) being changed to HKCGH (SEQ ID NO:58) as seen by comparing amino acids 105-109 of SEQ ID NO:10 (wild-type D form) to amino acids 105-109 of SEQ ID NO:12 (mutant D form). A similar mutation in other Fad-2 sequences is contemplated to result in a non-functional gene product. (Compare SEQ ID NO:2 to SEQ ID NO:4).

Please amend the paragraph beginning at page 10, line 3, as follows:

Among the types of mutations in an HECGH motif (SEQ ID NO:60) that render the resulting gene product non-functional are non-conservative substitutions. An illustrative example of a non-conservative substitution is substitution of a glycine residue for either the first or second histidine. Such a substitution replaces a charged residue (histidine) with a non-polar residue (glycine). Another type of mutation that renders the resulting gene product non-functional is an insertion mutation, e.g., insertion of a glycine between the cysteine and glutamic acid residues in the HECGH motif (SEQ ID NO:60).

Please amend the paragraph beginning at page 10, line 10, as follows below. Please note that the underlining in DRDYEILNKV is in the original application.

Other regions having suitable conserved amino acid motifs include the HRRHH motif (SEQ ID NO:61) shown in Table 2, the HRTHH motif (SEQ ID NO:62) shown in Table 6 and the HVAHH motif (SEQ ID NO:63) shown in Table 3. See, e.g., WO 94/15116; Hitz, W. et al., Plant Physiol., 105:635-641 (1994); Okuley, J., et al., supra; and Yadav, N. et al., supra. An illustrative example of a mutation in the region shown in Table 3 is a mutation at nucleotides corresponding to the codon for glycine (amino acid 303 of *B. napus*). A non-conservative Gly to Glu substitution results in the amino acid sequence DRDYGILNKV (SEQ ID NO:47; amino acids 299-308 of SEQ ID NO:14) being changed to sequence DRDYEILNKV (SEQ ID NO:50; amino acids 299-308 of SEQ ID NO:18) (compare wild-type F form SEQ ID NO:14 to mutant Q4275 SEQ ID NO:18, Fig. 3).

Please amend the paragraph beginning at page 10, line 19, as follows below. Please note that the underlining in KYHNNP is in the original application.

Another region suitable for a mutation in a delta-12 desaturase sequence contains the motif KYLNNP (SEQ ID NO:64) at nucleotides corresponding to amino acids ~~171~~ 170 to 175 of the *Brassica* desaturase sequence. An illustrative example of a mutation is this region is a Leu to His substitution, resulting in the amino acid sequence (Table 4) KYHNNP (SEQ ID NO:53; compare wild-type Fad2-F amino acids 170-175 of SEQ ID NO:14 to mutant Fad2-F amino acids 170-175 of SEQ ID NO:16). A similar mutation in other Fad-2 amino acid sequences is contemplated to result in a non-functional gene product. (Compare SEQ ID NO:6 to SEQ ID NO:8).

Please amend Table 1 at page 11 as follows below. Please note that the underlining in the table headers is present in the original application.

TABLE 1

Alignment of Amino Acid Sequences from Microsomal Delta-12 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana	100-129	IWVIAHECGH HAFSDYQWLD DTVGLIFHSF (SEQ ID NO:27)
Glycine max	96-125	VWVIAHECGH HAFSKYQWVD DVVGLTLHST (SEQ ID NO:28)
Zea mays	106-135	VWVIAHECGH HAFSDYSLLD DVVGLVLHSS (SEQ ID NO:29)
Ricinus communis[a]	1- 29	WVMAHDCGH HAFSDYQLLD DVVGLILHSC (SEQ ID NO:30)
Brassica napus D	100-128[b]	VWVIAHECGH HAFSDYQWLD DTVGLIFHS (SEQ ID NO:65)
Brassica napus F	100-128[c]	VWVIAHECGH HAFSDYQWLD DTVGLIFHS (SEQ ID NO:65)

[a] from plasmid pRF2-1C, [b]positions 100-128 of SEQ ID NO:10; [c]positions 100-128 of SEQ ID NO:14

Please amend Table 2 at page 11 as follows below. Please note that the underlining in the table headers is present in the original application.

TABLE 2

Alignment of Amino Acid Sequences from Microsomal Delta-12 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana	130-158	LLVPYFSWKY SHRRHHSNTG SLERDEVFV (SEQ ID NO:31)
Glycine max	126-154	LLVPYFSWKI SHRRHHSNTG SLDRDEVFV (SEQ ID NO:32)
Zea mays	136-164	LMVPYFSWKY SHRRHHSNTG SLERDEVFV (SEQ ID NO:33)
Ricinus communis[a]	30- 58	LLVPYFSWKH SHRRHHSNTG SLERDEVFV (SEQ ID NO:34)
Brassica napus D	130-158[b]	LLVPYFSWKY SHRRHHSNTG SLERDEVFV (SEQ ID NO:31)
Brassica napus F	130-158[c]	LLVPYFSWKY SHRRHHSNTG SLERDEVFV (SEQ ID NO:31)

[a] from plasmid pRF2-1C; [b]positions 130-158 of SEQ ID NO:10; [c]positions 130-158 of SEQ ID NO:14

Please amend Table 3 at page 11 as follows below. Please note that the underlining in the table headers is present in the original application.

TABLE 3

Alignment of Amino Acid Sequences from Microsomal Delta-12 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana	298-333	DRDYGILNKV FHNITDTHVA HHLFSTMPHY NAMEAT(SEQ ID NO:35)
Glycine max	294-329	DRDYGILNKV FHHITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:36)
Zea mays	305-340	DRDYGILNRV FHNITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:37)
Ricinus communis[a]	198-224	DRDYGILNKV FHNITDTQVA HHLF TMP(SEQ ID NO:38)
Brassica napus D	299-334[b]	DRDYGILNKV FHNITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:66)
Brassica napus F	299-334[c]	DRDYGILNKV FHNITDTHVA HHLFSTMPHY HAMEAT(SEQ ID NO:66)

[a] from plasmid pRF2-1C; [b]positions 299-334 of SEQ ID NO:10; [c]positions 299-334 of SEQ ID NO:14

Please amend Table 4 at page 11 as follows below. Please note that the underlining in the table headers is present in the original application.

TABLE 4

Alignment of Conserved Amino Acids from Microsomal Delta-12 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana	165-180	IKWYGKYLNN PLGRIM(SEQ ID NO:39)
Glycine max	161-176	VAWFSLYLNN PLGRAV(SEQ ID NO:40)
Zea mays	172-187	PWYTPYVYNN PVGRVV(SEQ ID NO:41)
Ricinus communis[a]	65- 80	IRWYSKYLNN PPGRIM(SEQ ID NO:42)
Brassica napus D	165-180[b]	IKWYGKYLNN PLGRTV(SEQ ID NO:67)
Brassica napus F	165-180[c]	IKWYGKYLNN PLGRTV(SEQ ID NO:67)

[a] from plasmid pRF2-1C; [b]positions 165-180 of SEQ ID NO:10; [c]positions 165-180 of SEQ ID NO:14

Please amend Table 5 at page 12 as follows below. Please note that the underlining in the table headers is present in the original application.

TABLE 5

Alignment of Conserved Amino Acids from Plastid and Microsomal Delta-15 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
Arabidopsis thaliana[a]	156-177	WALFVLGHD CGHGSFSNDP KLN(SEQ ID NO:43)
Brassica napus[a]	114-135	WALFVLGHD CGHGSFSNDP RLN(SEQ ID NO:44)
Glycine max[a]	164-185	WALFVLGHD CGHGSFSNNS KLN(SEQ ID NO:45)
Arabidopsis thaliana	94-115	WAIFVLGHD CGHGSFSDIP LLN(SEQ ID NO:46)
Brassica napus	87-109	WALFVLGHD CGHGSFSNDP RLN(SEQ ID NO:44)
Glycine max	93-114	WALFVLGHD CGHGSFSDSP PLN(SEQ ID NO:48)

[a] Plastid sequences

Please amend Table 6 at page 12 as follows below. Please note that the underlining in the table headers is present in the original application.

TABLE 6

Alignment of Conserved Amino Acids from Plastid and Microsomal Delta-15 Fatty Acid Desaturases

Species	Position	Amino Acid Sequence
A. thaliana[a]	188-216	ILVPYHGWRI SHRTHHQNHG HVENDESWH(SEQ ID NO:49)
B. napus[a]	146-174	ILVPYHGWRI SHRTHHQNHG HVENDESWH(SEQ ID NO:49)
Glycine max[a]	196-224	ILVPYHGWRI SHRTHHQHHG HAENDESWH(SEQ ID NO:51)
A. thaliana	126-154	ILVPYHGWRI SHRTHHQNHG HVENDESWV(SEQ ID NO:52)
Brassica napus	117-145	ILVPYHGWRI SHRTHHQNHG HVENDESWV(SEQ ID NO:52)
Glycine max	125-153	ILVPYHGWRI SHRTHHQNHG HIEKDESWV(SEQ ID NO:54)

[a] Plastid sequences

Please amend the paragraph beginning at page 14, line 3, as follows:

The seeds of several different fatty acid lines have been deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, Virginia 20110-2209, and have the following accession numbers.

Please amend Table 20 at page 40 as shown below. Please not that the only changes to this table occur in the column entitled Position. The underlining in the header and in the Sequence listings is present in the original application.

TABLE 20

Alignment of Amino Acid Sequences
of Cloned Canola Membrane Bound-Desaturases

Desaturase Gene	Sequence[a]	Position
Canola-fad2-D(mutant)	AH**K**CGH(SEQ ID NO:68)	109-114 of SEQ ID NO:12
Canola-Fad2-D	AHECGH(SEQ ID NO:59)	109-114 of SEQ ID NO:10
Canola-Fad2-F	AHECGH(SEQ ID NO:59)	109-114 of SEQ ID NO:14
Canola-FadC	GHDCAH (SEQ ID NO:55)	170-175
Canola-fad3 (mutant)	GH**K**CGH (SEQ ID NO:56)	94-99
Canola-Fad3	GHDCGH (SEQ ID NO:57)	94-99
Canola-FadD	GHDCGH (SEQ ID NO:57)	125-130

(FadD = Plastid delta 15, Fad3 = Microsomal delta-15),
(FadC = Plastid delta-12, Fad2 = Microsomal delta-12)

[a] One letter amino acid code; conservative substitutions are underlined; non-conservative substitutions are in bold.

Please amend the paragraph beginning at page 40, line 19, as follows:

Transcription in vivo was analyzed by RT-PCR analysis of stage II and stage III developing seeds and leaf tissue. The primers used to specifically amplify delta-12 desaturase F gene RNA from the indicated tissues were sense primer 5'-GGATATGATGATGGTGAAAGA-3' (SEQ ID NO:19) and antisense primer 5'-TCTTTCACCATCATCATATCC-3' (SEQ ID NO:20). The primers used to specifically amplify delta-12 desaturase D gene RNA from the indicated tissues were sense primer 5'-GTTATGAAGCAAAGAAGAAAC-3' (SEQ ID NO:21) and antisense primer 5'-GTTTCTTCTTTGCTTCATAAC-3' (SEQ ID NO:22). The results indicated that mRNA of both the D and F gene was expressed in seed and leaf tissues of IMC 129, Q508 and wild type Westar plants.

Please amend the paragraph beginning at page 44, line 22, as follows:

The Fad2-D gene was amplified once using Elongase® (Gibco-BRL). PCR primers were: 5'-CAUCAUCAUCAUCTTCTTCGTAGGGTTCATCG-3' (SEQ ID NO:23) and 5'-CUACUACUACUATCATAGAAGAGAAAGGTTCAG-3' (SEQ ID NO:24) for the 5' and 3' ends of the gene, respectively.

Please amend the paragraph beginning at page 44, line 26, as follows:

The Fad2-F gene was independently amplified 4 times, twice with Elongase® and twice with Taq polymerase (Boehringer Mannheim). The PCR primers used were: 5'CAUCAUCAUCAUCATGGGTGCACGTGGAAGAA3' (SEQ ID NO:25) and 5'CUACUACUACUATCTTTCACCATCATCATATCC3' (SEQ ID NO:26) for the 5' and 3' ends of the gene, respectively.

Please insert the sequence listing at the end of the application, pursuant to the attached Request to Transfer Computer Readable Form.